



SUBSTITUTE SEQUENCE LISTING

(1) GENERAL INFORMATION:

- al*
- (i) APPLICANT: PULST, STEFAN M.
 - (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR ATAXIA-2 AND PRODUCTS RELATED THERETO
 - (iii) NUMBER OF SEQUENCES: 18
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
 - (B) STREET: 119 NORTH FOURTH STREET, SUITE 203
 - (C) CITY: MINNEAPOLIS
 - (D) STATE: MINNESOTA
 - (E) COUNTRY: 55401
 - (F) ZIP: 55401
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/981,998
 - (B) FILING DATE: 11-MAY-1998
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO 97/42314
 - (B) FILING DATE: 08-MAY-1997
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/727,084
 - (B) FILING DATE: 08-OCT-1996
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/022,207
 - (B) FILING DATE: 19-JUL-1996
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/017,388
 - (B) FILING DATE: 08-MAY-1996
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: MUETING, ANN M.
 - (B) REGISTRATION NUMBER: 33,977
 - (C) REFERENCE/DOCKET NUMBER: 232.00010120
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612-305-1217
 - (B) TELEFAX: 612-305-1228

(2) INFORMATION FOR SEQ ID NO:1:

- a1
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGTAGCAA CGGAAACGGC GCGGCGCGCT TTCGGCCCGG CTCCCGGCGG CTCCTTGGTC	60
TCGGCGGGCC TCCCCGCCCC TTCGTCGTCG TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC	120
CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCG TCGTCCCCG CCGCGTTCCG	180
GCGTCTCCTT GGCGCGCCCG GCTCCCGGCT GTCCCCGCCC GCGGTGCGAG CCGGTGTATG	240
GGCCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC	300
AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA	360
AGCCCGGCGG CAGCGGCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCG TCCTCGTCCT	420
CGGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGGCG	480
GGAGGCCCGG CCTGGGCAGG TGGGTGTCGG CACCCC	516

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 163..4101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACCCCCGAGA AAGCAACCCA GCGCGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG	60
GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CGGTAAAGAG TCCCTATCCG	120
CACCTCCGCT CCCACCCGGC GCCTCGGCGC GCCCGCCCTC CG ATG CGC TCA GCG	174
Met Arg Ser Ala	

91
cont

GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC	222
Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe	
5 10 15 20	
GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG	270
Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg	
25 30 35	
CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC	318
Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser	
40 45 50	
GCC GCC CCT CCC CCG CCC GGC CCC GGC CCC CCT CCC TCC CGG CAG AGC	366
Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro Ser Arg Gln Ser	
55 60 65	
TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC	414
Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly	
70 75 80	
GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG CCT	462
Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Gly Pro	
85 90 95 100	
CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC	510
Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala	
105 110 115	
CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC	558
Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser	
120 125 130	
CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC	606
Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys Pro	
135 140 145	
CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG AAG	654
Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu Lys	
150 155 160	
CCC CAG CAG CAG CAG CAG CAG CAG CAG CAA CAG CAG CAG CAG CAA CAG	702
Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln	
165 170 175 180	
CAG CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT GTC CGC	750
Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala Ala Asn Val Arg	
185 190 195	
AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCC GCG CCT TCG	798
Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Ala Pro Ser	
200 205 210	
CCG TCC TCG TCC TCG GTC TCC TCG TCC TCG GCC ACG GCT CCC TCC TCG	846
Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala Thr Ala Pro Ser Ser	
215 220 225	

21
 Conf

GTG	GTC	GCG	GCG	ACC	TCC	GGC	GGC	GGG	AGG	CCC	GGC	CTG	GGC	AGA	GGT	894
Val	Val	Ala	Ala	Thr	Ser	Gly	Gly	Gly	Arg	Pro	Gly	Leu	Gly	Arg	Gly	
	230					235					240					
CGA	AAC	AGT	AAC	AAA	GGA	CTG	CCT	CAG	TCT	ACG	ATT	TCT	TTT	GAT	GGA	942
Arg	Asn	Ser	Asn	Lys	Gly	Leu	Pro	Gln	Ser	Thr	Ile	Ser	Phe	Asp	Gly	
245					250					255					260	
ATC	TAT	GCA	AAT	ATG	AGG	ATG	GTT	CAT	ATA	CTT	ACA	TCA	GTT	GTT	GGC	990
Ile	Tyr	Ala	Asn	Met	Arg	Met	Val	His	Ile	Leu	Thr	Ser	Val	Val	Gly	
				265					270					275		
TCC	AAA	TGT	GAA	GTA	CAA	GTG	AAA	AAT	GGA	GGT	ATA	TAT	GAA	GGA	GTT	1038
Ser	Lys	Cys	Glu	Val	Gln	Val	Lys	Asn	Gly	Gly	Ile	Tyr	Glu	Gly	Val	
			280					285					290			
TTT	AAA	ACT	TAC	AGT	CCG	AAG	TGT	GAT	TTG	GTA	CTT	GAT	GCC	GCA	CAT	1086
Phe	Lys	Thr	Tyr	Ser	Pro	Lys	Cys	Asp	Leu	Val	Leu	Asp	Ala	Ala	His	
		295					300					305				
GAG	AAA	AGT	ACA	GAA	TCC	AGT	TCG	GGG	CCG	AAA	CGT	GAA	GAA	ATA	ATG	1134
Glu	Lys	Ser	Thr	Glu	Ser	Ser	Ser	Gly	Pro	Lys	Arg	Glu	Glu	Ile	Met	
	310					315					320					
GAG	AGT	ATT	TTG	TTC	AAA	TGT	TCA	GAC	TTT	GTT	GTG	GTA	CAG	TTT	AAA	1182
Glu	Ser	Ile	Leu	Phe	Lys	Cys	Ser	Asp	Phe	Val	Val	Val	Gln	Phe	Lys	
325					330					335					340	
GAT	ATG	GAC	TCC	AGT	TAT	GCA	AAA	AGA	GAT	GCT	TTT	ACT	GAC	TCT	GCT	1230
Asp	Met	Asp	Ser	Ser	Tyr	Ala	Lys	Arg	Asp	Ala	Phe	Thr	Asp	Ser	Ala	
				345					350					355		
ATC	AGT	GCT	AAA	GTG	AAT	GGC	GAA	CAC	AAA	GAG	AAG	GAC	CTG	GAG	CCC	1278
Ile	Ser	Ala	Lys	Val	Asn	Gly	Glu	His	Lys	Glu	Lys	Asp	Leu	Glu	Pro	
			360					365					370			
TGG	GAT	GCA	GGT	GAA	CTC	ACA	GCC	AAT	GAG	GAA	CTT	GAG	GCT	TTG	GAA	1326
Trp	Asp	Ala	Gly	Glu	Leu	Thr	Ala	Asn	Glu	Glu	Leu	Glu	Ala	Leu	Glu	
		375					380					385				
AAT	GAC	GTA	TCT	AAT	GGA	TGG	GAT	CCC	AAT	GAT	ATG	TTT	CGA	TAT	AAT	1374
Asn	Asp	Val	Ser	Asn	Gly	Trp	Asp	Pro	Asn	Asp	Met	Phe	Arg	Tyr	Asn	
	390					395					400					
GAA	GAA	AAT	TAT	GGT	GTA	GTG	TCT	ACG	TAT	GAT	AGC	AGT	TTA	TCT	TCG	1422
Glu	Glu	Asn	Tyr	Gly	Val	Val	Ser	Thr	Tyr	Asp	Ser	Ser	Leu	Ser	Ser	
405					410					415					420	
TAT	ACA	GTG	CCC	TTA	GAA	AGA	GAT	AAC	TCA	GAA	GAA	TTT	TTA	AAA	CGG	1470
Tyr	Thr	Val	Pro	Leu	Glu	Arg	Asp	Asn	Ser	Glu	Glu	Phe	Leu	Lys	Arg	
				425					430					435		
GAA	GCA	AGG	GCA	AAC	CAG	TTA	GCA	GAA	GAA	ATT	GAG	TCA	AGT	GCC	CAG	1518
Glu	Ala	Arg	Ala	Asn	Gln	Leu	Ala	Glu	Glu	Ile	Glu	Ser	Ser	Ala	Gln	
			440					445					450			

TAC AAA GCT CGA GTG GCC CTG GAA AAT GAT GAT AGG AGT GAG GAA GAA 1566
 Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu
 455 460 465

AAA TAC ACA GCA GTT CAG AGA AAT TCC AGT GAA CGT GAG GGG CAC AGC 1614
 Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg Glu Gly His Ser
 470 475 480

ATA AAC ACT AGG GAA AAT AAA TAT ATT CCT CCT GGA CAA AGA AAT AGA 1662
 Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg
 485 490 495 500

GAA GTC ATA TCC TGG GGA AGT GGG AGA CAG AAT TCA CCG CGT ATG GGC 1710
 Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser Pro Arg Met Gly
 505 510 515

CAG CCT GGA TCG GGC TCC ATG CCA TCA AGA TCC ACT TCT CAC ACT TCA 1758
 Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr Ser His Thr Ser
 520 525 530

GAT TTC AAC CCG AAT TCT GGT TCA GAC CAA AGA GTA GTT AAT GGA GGT 1806
 Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val Val Asn Gly Gly
 535 540 545

GTT CCC TGG CCA TCG CCT TGC CCA TCT CCT TCC TCT CGC CCA CCT TCT 1854
 Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser Arg Pro Pro Ser
 550 555 560

CGC TAC CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC ACC CCT 1902
 Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr Pro
 565 570 575 580

ACA CGG CCG CCC TCC AGG CCC CCC TCG CGG CCA TCC AGA CCC CCG TCT 1950
 Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser
 585 590 595

CAC CCC TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG CCT AAA 1998
 His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys
 600 605 610

CGC ATG TCT TCA GAA GGG CCT CCA AGG ATG TCC CCA AAG GCC CAG CGA 2046
 Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg
 615 620 625

CAT CCT CGA AAT CAC AGA GTT TCT GCT GGG AGG GGT TCC ATA TCC AGT 2094
 His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Ile Ser Ser
 630 635 640

GGC CTA GAA TTT GTA TCC CAC AAC CCA CCC AGT GAA GCA GCT ACT CCT 2142
 Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala Thr Pro
 645 650 655 660

CCA GTA GCA AGG ACC AGT CCC TCG GGG GGA ACG TGG TCA TCA GTG GTC 2190
 Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp Ser Ser Val Val
 665 670 675

AGT GGG GTT CCA AGA TTA TCC CCT AAA ACT CAT AGA CCC AGG TCT CCC	2238
Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro	
680 685 690	
AGA CAG AAC AGT ATT GGA AAT ACC CCC AGT GGG CCA GTT CTT GCT TCT	2286
Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro Val Leu Ala Ser	
695 700 705	
CCC CAA GCT GGT ATT ATT CCA ACT GAA GCT GTT GCC ATG CCT ATT CCA	2334
Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala Met Pro Ile Pro	
710 715 720	
GCT GCA TCT CCT ACG CCT GCT AGT CCT GCA TCG AAC AGA GCT GTT ACC	2382
Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala Val Thr	
725 730 735 740	
CCT TCT AGT GAG GCT AAA GAT TCC AGG CTT CAA GAT CAG AGG CAG AAC	2430
Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg Gln Asn	
745 750 755	
TCT CCT GCA GGG AAT AAA GAA AAT ATT AAA CCC AAT GAA ACA TCA CCT	2478
Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn Glu Thr Ser Pro	
760 765 770	
AGC TTC TCA AAA GCT GAA AAC AAA GGT ATA TCA CCA GTT GTT TCT GAA	2526
Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro Val Val Ser Glu	
775 780 785	
CAT AGA AAA CAG ATT GAT GAT TTA AAG AAA TTT AAG AAT GAT TTT AGG	2574
His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp Phe Arg	
790 795 800	
TTA CAG CCA AGT TCT ACT TCT GAA TCT ATG GAT CAA CTA CTA AAC AAA	2622
Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu Asn Lys	
805 810 815 820	
AAT AGA GAG GGA GAA AAA TCA AGA GAT TTG ATC AAA GAC AAA ATT GAA	2670
Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys Ile Glu	
825 830 835	
CCA AGT GCT AAG GAT TCT TTC ATT GAA AAT AGC AGC AGC AAC TGT ACC	2718
Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser Ser Asn Cys Thr	
840 845 850	
AGT GGC AGC AGC AAG CCG AAT AGC CCC AGC ATT TCC CCT TCA ATA CTT	2766
Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser Pro Ser Ile Leu	
855 860 865	
AGT AAC ACG GAG CAC AAG AGG GGA CCT GAG GTC ACT TCC CAA GGG GTT	2814
Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln Gly Val	
870 875 880	
CAG ACT TCC AGC CCA GCA TGT AAA CAA GAG AAA GAC GAT AAG GAA GAG	2862
Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Lys Glu Glu	
885 890 895 900	

AAG AAA GAC GCA GCT GAG CAA GTT AGG AAA TCA ACA TTG AAT CCC AAT	2910
Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr Leu Asn Pro Asn	
905 910 915	
GCA AAG GAG TTC AAC CCA CGT TCC TTC TCT CAG CCA AAG CCT TCT ACT	2958
Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro Ser Thr	
920 925 930	
ACC CCA ACT TCA CCT CGG CCT CAA GCA CAA CCT AGC CCA TCT ATG GTG	3006
Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser Met Val	
935 940 945	
GGT CAT CAA CAG CCA ACT CCA GTT TAT ACT CAG CCT GTT TGT TTT GCA	3054
Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro Val Cys Phe Ala	
950 955 960	
CCA AAT ATG ATG TAT CCA GTC CCA GTG AGC CCA GGC GTG CAA CCT TTA	3102
Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln Pro Leu	
965 970 975 980	
TAC CCA ATA CCT ATG ACG CCC ATG CCA GTG AAT CAA GCC AAG ACA TAT	3150
Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys Thr Tyr	
985 990 995	
AGA GCA GTA CCA AAT ATG CCC CAA CAG CGG CAA GAC CAG CAT CAT CAG	3198
Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp Gln His His Gln	
1000 1005 1010	
AGT GCC ATG ATG CAC CCA GCG TCA GCA GCG GGC CCA CCG ATT GCA GCC	3246
Ser Ala Met Met His Pro Ala Ser Ala Ala Gly Pro Pro Ile Ala Ala	
1015 1020 1025	
ACC CCA CCA GCT TAC TCC ACG CAA TAT GTT GCC TAC AGT CCT CAG CAG	3294
Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr Ser Pro Gln Gln	
1030 1035 1040	
TTC CCA AAT CAG CCC CTT GTT CAG CAT GTG CCA CAT TAT CAG TCT CAG	3342
Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His Tyr Gln Ser Gln	
1045 1050 1055 1060	
CAT CCT CAT GTC TAT AGT CCT GTA ATA CAG GGT AAT GCT AGA ATG ATG	3390
His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn Ala Arg Met Met	
1065 1070 1075	
GCA CCA CCA ACA CAC GCC CAG CCT GGT TTA GTA TCT TCT TCA GCA ACT	3438
Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser Ser Ser Ala Thr	
1080 1085 1090	
CAG TAC GGG GCT CAT GAG CAG ACG CAT GCG ATG TAT GCA TGT CCC AAA	3486
Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr Ala Cys Pro Lys	
1095 1100 1105	
TTA CCA TAC AAC AAG GAG ACA AGC CCT TCT TTC TAC TTT GCC ATT TCC	3534
Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr Phe Ala Ile Ser	
1110 1115 1120	

ACG GGC TCC CTT GCT CAG CAG TAT GCG CAC CCT AAC GCT ACC CTG CAC Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn Ala Thr Leu His 1125 1130 1135 1140	3582
CCA CAT ACT CCA CAC CCT CAG CCT TCA GCT ACC CCC ACT GGA CAG CAG Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro Thr Gly Gln Gln 1145 1150 1155	3630
CAA AGC CAA CAT GGT GGA AGT CAT CCT GCA CCC AGT CCT GTT CAG CAC Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser Pro Val Gln His 1160 1165 1170	3678
CAT CAG CAC CAG GCC GCC CAG GCT CTC CAT CTG GCC AGT CCA CAG CAG His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala Ser Pro Gln Gln 1175 1180 1185	3726
CAG TCA GCC ATT TAC CAC GCG GGG CTT GCG CCA ACT CCA CCC TCC ATG Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr Pro Pro Ser Met 1190 1195 1200	3774
ACA CCT GCC TCC AAC ACG CAG TCG CCA CAG AAT AGT TTC CCA GCA GCA Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser Phe Pro Ala Ala 1205 1210 1215 1220	3822
CAA CAG ACT GTC TTT ACG ATC CAT CCT TCT CAC GTT CAG CCG GCG TAT Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val Gln Pro Ala Tyr 1225 1230 1235	3870
ACC AAC CCA CCC CAC ATG GCC CAC GTA CCT CAG GCT CAT GTA CAG TCA Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala His Val Gln Ser 1240 1245 1250	3918
GGA ATG GTT CCT TCT CAT CCA ACT GCC CAT GCG CCA ATG ATG CTA ATG Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro Met Met Leu Met 1255 1260 1265	3966
ACG ACA CAG CCA CCC GGC GGT CCC CAG GCC GCC CTC GCT CAA AGT GCA Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu Ala Gln Ser Ala 1270 1275 1280	4014
CTA CAG CCC ATT CCA GTC TCG ACA ACA GCG CAT TTC CCC TAT ATG ACG Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro Tyr Met Thr 1285 1290 1295 1300	4062
CAC CCT TCA GTA CAA GCC CAC CAC CAA CAG CAG TTG TAA GGCTGCCCTG His Pro Ser Val Gln Ala His His Gln Gln Gln Leu *	4111
	1305 1310
GAGGAACCGA AAGGCCAAAT TCCCTCCTCC CTTCTACTGC TTCTACCAAC TGGAAGCACA	4171
GAAAACTAGA ATTTTCATTTA TTTTGTTTTT AAAATATATA TGTTGATTTC TTGTAACATC	4231
CAATAGGAAT GCTAACAGTT CACTTGCAGT GGAAGATACT TGGACCGAGT AGAGGCATTT	4291
AGGAACTTGG GGGCTATTCC ATAATTCCAT ATGCTGTTTC AGAGTCCCGC AGGTACCCCA	4351
GCTCTGCTTG CCGAAACTGG AAGTTATTTA TTTTTTAATA ACCCTTGAAA GTCATGAACA	4411

CATCAGCTAG CAAAAGAAGT AACAAGAGTG ATTCTTGCTG CTATTACTGC TAAAAAATAA 4471
 AAAAAAATAA 4481

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Arg	Ser	Ala	Ala	Ala	Ala	Pro	Arg	Ser	Pro	Ala	Val	Ala	Thr	Glu	
1					5				10					15		
Ser	Arg	Arg	Phe	Ala	Ala	Ala	Arg	Trp	Pro	Gly	Trp	Arg	Ser	Leu	Gln	
			20					25					30			
Arg	Pro	Ala	Arg	Arg	Ser	Gly	Arg	Gly	Gly	Gly	Gly	Ala	Ala	Pro	Gly	
			35				40						45			
Pro	Tyr	Pro	Ser	Ala	Ala	Pro	Pro	Pro	Pro	Gly	Pro	Gly	Pro	Pro	Pro	
	50					55					60					
Ser	Arg	Gln	Ser	Ser	Pro	Pro	Ser	Ala	Ser	Asp	Cys	Phe	Gly	Ser	Asn	
	65				70					75					80	
Gly	Asn	Gly	Gly	Gly	Ala	Phe	Arg	Pro	Gly	Ser	Arg	Arg	Leu	Leu	Gly	
				85					90					95		
Leu	Gly	Gly	Pro	Pro	Arg	Pro	Phe	Val	Val	Val	Leu	Leu	Pro	Leu	Ala	
			100					105					110			
Ser	Pro	Gly	Ala	Pro	Pro	Ala	Ala	Pro	Thr	Arg	Ala	Ser	Pro	Leu	Gly	
		115					120					125				
Ala	Arg	Ala	Ser	Pro	Pro	Arg	Ser	Gly	Val	Ser	Leu	Ala	Arg	Pro	Ala	
		130				135					140					
Pro	Gly	Cys	Pro	Arg	Pro	Ala	Cys	Glu	Pro	Val	Tyr	Gly	Pro	Leu	Thr	
	145				150					155				160		
Met	Ser	Leu	Lys	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	
				165				170						175		
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Ala	Ala	
				180				185					190			
Ala	Asn	Val	Arg	Lys	Pro	Gly	Gly	Ser	Gly	Leu	Leu	Ala	Ser	Pro	Ala	
		195				200						205				
Ala	Ala	Pro	Ser	Pro	Ser	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ser	Ala	Thr	
	210					215				220						

Ala Pro Ser Ser Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly
 225 230 235 240
 Leu Gly Arg Gly Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile
 245 250 255
 Ser Phe Asp Gly Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr
 260 265 270
 Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile
 275 280 285
 Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu
 290 295 300
 Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg
 305 310 315 320
 Glu Glu Ile Met Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val
 325 330 335
 Val Gln Phe Lys Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe
 340 345 350
 Thr Asp Ser Ala Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys
 355 360 365
 Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu
 370 375 380
 Glu Ala Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met
 385 390 395 400
 Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser
 405 410 415
 Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu
 420 425 430
 Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu
 435 440 445
 Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg
 450 455 460
 Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg
 465 470 475 480
 Glu Gly His Ser Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly
 485 490 495
 Gln Arg Asn Arg Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser
 500 505 510
 Pro Arg Met Gly Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr
 515 520 525

Ser His Thr Ser Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val
 530 535 540
 Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser
 545 550 555 560
 Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg
 565 570 575
 Ala Ala Thr Pro Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser
 580 585 590
 Arg Pro Pro Ser His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser
 595 600 605
 Thr Met Pro Lys Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro
 610 615 620
 Lys Ala Gln Arg His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly
 625 630 635 640
 Ser Ile Ser Ser Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu
 645 650 655
 Ala Ala Thr Pro Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp
 660 665 670
 Ser Ser Val Val Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg
 675 680 685
 Pro Arg Ser Pro Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro
 690 695 700
 Val Leu Ala Ser Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala
 705 710 715 720
 Met Pro Ile Pro Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn
 725 730 735
 Arg Ala Val Thr Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp
 740 745 750
 Gln Arg Gln Asn Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn
 755 760 765
 Glu Thr Ser Pro Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro
 770 775 780
 Val Val Ser Glu His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys
 785 790 795 800
 Asn Asp Phe Arg Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln
 805 810 815
 Leu Leu Asn Lys Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys
 820 825 830

Asp Lys Ile Glu Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser
 835 840 845
 Ser Asn Cys Thr Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser
 850 855 860
 Pro Ser Ile Leu Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr
 865 870 875 880
 Ser Gln Gly Val Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp
 885 890 895
 Asp Lys Glu Glu Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr
 900 905 910
 Leu Asn Pro Asn Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro
 915 920 925
 Lys Pro Ser Thr Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser
 930 935 940
 Pro Ser Met Val Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro
 945 950 955 960
 Val Cys Phe Ala Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly
 965 970 975
 Val Gln Pro Leu Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln
 980 985 990
 Ala Lys Thr Tyr Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp
 995 1000 1005
 Gln His His Gln Ser Ala Met Met His Pro Ala Ser Ala Ala Gly Pro
 1010 1015 1020
 Pro Ile Ala Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr
 1025 1030 1035 1040
 Ser Pro Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His
 1045 1050 1055
 Tyr Gln Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn
 1060 1065 1070
 Ala Arg Met Met Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser
 1075 1080 1085
 Ser Ser Ala Thr Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr
 1090 1095 1100
 Ala Cys Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr
 1105 1110 1115 1120
 Phe Ala Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn
 1125 1130 1135

Ala Thr Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro
1140 1145 1150

Thr Gly Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser
1155 1160 1165

Pro Val Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala
1170 1175 1180

Ser Pro Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr
1185 1190 1195 1200

Pro Pro Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser
1205 1210 1215

Phe Pro Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val
1220 1225 1230

Gln Pro Ala Tyr Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala
1235 1240 1245

His Val Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro
1250 1255 1260

Met Met Leu Met Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu
1265 1270 1275 1280

Ala Gln Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe
1285 1290 1295

Pro Tyr Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu
1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3798 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 50..3457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGCACGAGGT CCCC GCCCGG CGT GCGAGCC GGTGTATGGG CCGCTCACC ATG TCG
Met Ser
1

55

CTG AAG CCG CAG CCG CAG CCG CCC GCG CCC GCC ACT GGC CGC AAG CCC	103
Leu Lys Pro Gln Pro Gln Pro Pro Ala Pro Ala Thr Gly Arg Lys Pro	
5 10 15	
GGC GGC GGC CTG CTC TCG TCG CCC GGC GCC GCG CCG GCC TCG GCC GCG	151
Gly Gly Gly Leu Leu Ser Ser Pro Gly Ala Ala Pro Ala Ser Ala Ala	
20 25 30	
GTG ACC TCG GCT TCC GTG GTG CCG GCC CCG GCC GCG CCG GTG GCG TCT	199
Val Thr Ser Ala Ser Val Val Pro Ala Pro Ala Ala Pro Val Ala Ser	
35 40 45 50	
TCC TCG GCG GCC GCG GGC GGC GGG CGT CCC GGC CTG GGC AGA GGT CGG	247
Ser Ser Ala Ala Ala Gly Gly Gly Arg Pro Gly Leu Gly Arg Gly Arg	
55 60 65	
AAC AGT AGC AAA GGA CTG CCT CAG CCT ACG ATT TCT TTT GAT GGA ATC	295
Asn Ser Ser Lys Gly Leu Pro Gln Pro Thr Ile Ser Phe Asp Gly Ile	
70 75 80	
TAT GCA AAC GTG AGG ATG GTT CAT ATA CTT ACG TCA GTT GTT GGA TCG	343
Tyr Ala Asn Val Arg Met Val His Ile Leu Thr Ser Val Val Gly Ser	
85 90 95	
AAA TGT GAA GTA CAA GTG AAA AAC GGA GGC ATA TAT GAA GGA GTT TTT	391
Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly Val Phe	
100 105 110	
AAA ACA TAC AGT CCT AAG TGT GAC TTG GTA CTT GAT GCT GCA CAT GAG	439
Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His Glu	
115 120 125 130	
AAA AGT ACA GAA TCC AGT TCG GGG CCA AAA CGT GAA GAA ATA ATG GAG	487
Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg Glu Glu Ile Met Glu	
135 140 145	
AGT GTT TTG TTC AAA TGC TCA GAC TTC GTT GTG GTA CAG TTT AAA GAT	535
Ser Val Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys Asp	
150 155 160	
ACA GAC TCC AGT TAT GCA CGG AGA GAT GCT TTT ACT GAC TCT GCT CTC	583
Thr Asp Ser Ser Tyr Ala Arg Arg Asp Ala Phe Thr Asp Ser Ala Leu	
165 170 175	
AGC GCA AAG GTG AAT GGT GAG CAC AAG GAG AAG GAC CTG GAG CCC TGG	631
Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro Trp	
180 185 190	
GAT GCA GGG GAG CTC ACG GCC AGC GAG GAG CTG GAG CTG GAG AAT GAT	679
Asp Ala Gly Glu Leu Thr Ala Ser Glu Glu Leu Glu Leu Glu Asn Asp	
195 200 205 210	
GTG TCT AAT GGA TGG GAC CCC AAT GAC ATG TTT CGA TAT AAT GAA GAG	727
Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn Glu Glu	
215 220 225	

AAT TAT GGT GTG GTG TCC ACA TAT GAT AGC AGT TTA TCT TCA TAT ACG	775
Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser Tyr Thr	
230 235 240	
GTT CCT TTA GAA AGG GAC AAC TCA GAA GAA TTT CTT AAA CGG GAG GCA	823
Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg Glu Ala	
245 250 255	
AGG GCA AAC CAG TTA GCA GAA GAA ATT GAA TCC AGT GCT CAG TAC AAA	871
Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln Tyr Lys	
260 265 270	
GCT CGT GTC GCC CTT GAG AAT GAT GAC CGG AGT GAG GAA GAA AAA TAC	919
Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu Lys Tyr	
275 280 285 290	
ACA GCA GTC CAG AGA AAC TGC AGT GAC CGG GAG GGG CAT GGC CCC AAC	967
Thr Ala Val Gln Arg Asn Cys Ser Asp Arg Glu Gly His Gly Pro Asn	
295 300 305	
ACT AGG GAC AAT AAA TAT ATT CCT CCT GGA CAA AGA AAC AGA GAA GTC	1015
Thr Arg Asp Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg Glu Val	
310 315 320	
CTA TCC TGG GGA AGT GGG AGA CAG AGC TCA CCA CGG ATG GGC CAG CCT	1063
Leu Ser Trp Gly Ser Gly Arg Gln Ser Ser Pro Arg Met Gly Gln Pro	
325 330 335	
GGG CCA GGC TCC ATG CCG TCA AGA GCT GCT TCT CAC ACT TCA GAT TTC	1111
Gly Pro Gly Ser Met Pro Ser Arg Ala Ala Ser His Thr Ser Asp Phe	
340 345 350	
AAC CCG AAC GCT GGC TCA GAC CAA AGA GTA GTT AAT GGA GGT GTT CCC	1159
Asn Pro Asn Ala Gly Ser Asp Gln Arg Val Val Asn Gly Gly Val Pro	
355 360 365 370	
TGG CCA TCG CCT TGC CCA TCT CAT TCC TCT CGC CCA CCT TCT CGC TAC	1207
Trp Pro Ser Pro Cys Pro Ser His Ser Ser Arg Pro Pro Ser Arg Tyr	
375 380 385	
CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC ACC CAT ACA CGG	1255
Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr His Thr Arg	
390 395 400	
CCG CCC TCC AGG CCC CCC TCG AGG CCA TCC AGA CCC CCG TCT CAC CCC	1303
Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser His Pro	
405 410 415	
TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG CCT AAA CGC ATG	1351
Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys Arg Met	
420 425 430	
TCT TCA GAA GGA CCC CCA AGG ATG TCT CCA AAG GCA CAG CGC CAC CCT	1399
Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg His Pro	
435 440 445 450	

CGG AAT CAC AGA GTC TCT GCT GGG AGA GGC TCC ATG TCT AGT GGC CTA	1447
Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Met Ser Ser Gly Leu	
455 460 465	
GAA TTT GTA TCC CAC AAT CCC CCA AGT GAA GCA GCT GCT CCT CCA GTG	1495
Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala Ala Pro Pro Val	
470 475 480	
GCA AGG ACC AGT CCT GCA GGG GGA ACG TGG TCC TCA GTG GTC AGT GGG	1543
Ala Arg Thr Ser Pro Ala Gly Gly Thr Trp Ser Ser Val Val Ser Gly	
485 490 495	
GTT CCA AGG TTA TCT CCC AAA ACT CAC AGA CCC AGG TCT CCC AGG CAG	1591
Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro Arg Gln	
500 505 510	
AGC AGC ATT GGA AAC TCT CCC AGC GGG CCT GTG CTT GCT TCT CCC CAA	1639
Ser Ser Ile Gly Asn Ser Pro Ser Gly Pro Val Leu Ala Ser Pro Gln	
515 520 525 530	
GCT GGC ATC ATC CCT GCA GAA GCC GTT TCC ATG CCT GTT CCC GCC GCA	1687
Ala Gly Ile Ile Pro Ala Glu Ala Val Ser Met Pro Val Pro Ala Ala	
535 540 545	
TCT CCG ACT CCT GCC AGC CCT GCA TCC AAC AGA GCA CTG ACC CCA TCT	1735
Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala Leu Thr Pro Ser	
550 555 560	
ATT GAG GCA AAA GAT TCC AGG CTT CAA GAT CAG AGG CAG AAC TCT CCT	1783
Ile Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg Gln Asn Ser Pro	
565 570 575	
GCA GGG AGT AAA GAA AAT GTT AAA GCA AGT GAA ACA TCA CCT AGC TTT	1831
Ala Gly Ser Lys Glu Asn Val Lys Ala Ser Glu Thr Ser Pro Ser Phe	
580 585 590	
TCA AAA GCT GAC AAC AAA GGT ATG TCA CCA GTT GTT TCT GAA CAC AGA	1879
Ser Lys Ala Asp Asn Lys Gly Met Ser Pro Val Val Ser Glu His Arg	
595 600 605 610	
AAA CAG ATT GAT GAC TTA AAG AAG TTT AAG AAT GAT TTT AGG TTA CAG	1927
Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp Phe Arg Leu Gln	
615 620 625	
CCA AGC TCT ACA TCT GAA TCT ATG GAT CAA CTA CTA AGC AAA AAT AGA	1975
Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu Ser Lys Asn Arg	
630 635 640	
GAA GGA GAA AAG TCA CGA GAT TTG ATT AAA GAT AAA ACG GAA GCA AGT	2023
Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys Thr Glu Ala Ser	
645 650 655	
GCT AAG GAT AGT TTC ATT GAC AGC AGC AGC AGC AGC AGC AAC TGT ACC	2071
Ala Lys Asp Ser Phe Ile Asp Ser Ser Ser Ser Ser Ser Asn Cys Thr	
660 665 670	

AGT GGC AGC AGC AAG ACC AAC AGC CCT AGC ATC TCC CCT TCC ATG CTT	2119
Ser Gly Ser Ser Lys Thr Asn Ser Pro Ser Ile Ser Pro Ser Met Leu	
675 680 685 690	
AGT AAT GCA GAG CAC AAG AGG GGG CCT GAG GTC ACA TCC CAA GGG GTG	2167
Ser Asn Ala Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln Gly Val	
695 700 705	
CAG ACT TCC AGC CCA GCC TGC AAA CAA GAG AAG GAT GAC AGA GAA GAG	2215
Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Arg Glu Glu	
710 715 720	
AAG AAA GAC ACA ACA GAG CAG GTT AGG AAA TCG ACA TTG AAT CCC AAT	2263
Lys Lys Asp Thr Thr Glu Gln Val Arg Lys Ser Thr Leu Asn Pro Asn	
725 730 735	
GCA AAG GAG TTC AAC CCT CGT TCT TTC TCT CAG CCA AAG CCT TCT ACT	2311
Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro Ser Thr	
740 745 750	
ACC CCA ACG TCA CCT CGG CCT CAA GCA CAA CCC AGC CCA TCT ATG GTG	2359
Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser Met Val	
755 760 765 770	
GGT CAT CAG CAG CCA GCT CCA GTG TAC ACT CAG CCT GTG TGC TTC GCA	2407
Gly His Gln Gln Pro Ala Pro Val Tyr Thr Gln Pro Val Cys Phe Ala	
775 780 785	
CCC AAT ATG ATG TAT CCC GTC CCA GTG AGC CCG GGC GTA CAA CCT TTA	2455
Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln Pro Leu	
790 795 800	
TAC CCA ATA CCT ATG ACG CCC ATG CCT GTG AAC CAA GCC AAG ACA TAT	2503
Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys Thr Tyr	
805 810 815	
AGA GCA GGT AAA GTA CCA AAT ATG CCC CAA CAG CGA CAA GAC CAA CAT	2551
Arg Ala Gly Lys Val Pro Asn Met Pro Gln Gln Arg Gln Asp Gln His	
820 825 830	
CAT CAA AGC ACC ATG ATG CAC CCA GCC TCC GCG GCA GGG CCA CCC ATC	2599
His Gln Ser Thr Met Met His Pro Ala Ser Ala Ala Gly Pro Pro Ile	
835 840 845 850	
GTA GCC ACC CCG CCC GCT TAC TCC ACT CAG TAC GTT GCC TAC AGC CCT	2647
Val Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr Ser Pro	
855 860 865	
CAG CAG TTT CCC AAT CAG CCT TTG GTC CAG CAT GTG CCG CAT TAT CAG	2695
Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His Tyr Gln	
870 875 880	
TCT CAG CAT CCT CAT GTG TAC AGT CCT GTC ATA CAA GGT AAT GCC AGG	2743
Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn Ala Arg	
885 890 895	

ATG ATG GCA CCA CCA GCA CAT GCT CAG CCT GGT TTA GTG TCT TCT TCA	2791
Met Met Ala Pro Pro Ala His Ala Gln Pro Gly Leu Val Ser Ser Ser	
900 905 910	
GCT GCT CAG TTC GGG GCT CAC GAG CAG ACG CAC GCC ATG TAT GCA TGT	2839
Ala Ala Gln Phe Gly Ala His Glu Gln Thr His Ala Met Tyr Ala Cys	
915 920 925 930	
CCC AAA TTA CCA TAC AAC AAG GAG ACA AGC CCT TCT TTC TAC TTT GCC	2887
Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr Phe Ala	
935 940 945	
ATT TCC ACC GGC TCC CTC GCT CAG CAG TAT GCA CAT CCT AAT GCC GCC	2935
Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn Ala Ala	
950 955 960	
CTG CAT CCA CAT ACT CCC CAT CCT CAG CCT TCG GCC ACT CCC ACC GGA	2983
Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro Thr Gly	
965 970 975	
CAG CAG CAA AGC CAG CAT GGT GGA AGT CAC CCT GCA CCC AGT CCT GTT	3031
Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser Pro Val	
980 985 990	
CAG CAC CAT CAG CAC CAG GCT GCC CAG GCT CTT CAT CTG GCC AGT CCA	3079
Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala Ser Pro	
995 1000 1005 1010	
CAG CAG CAG TCG GCC ATT TAT CAT GCG GGG CTG GCA CCA ACA CCA CCT	3127
Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr Pro Pro	
1015 1020 1025	
TCC ATG ACA CCT GCC TCT AAT ACA CAG TCT CCA CAG AGC AGT TTC CCA	3175
Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Ser Ser Phe Pro	
1030 1035 1040	
GCA GCA CAA CAG ACA GTC TTC ACC ATC CAC CCT TCT CAT GTT CAG CCG	3223
Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val Gln Pro	
1045 1050 1055	
GCA TAC ACC ACC CCA CCC CAC ATG GCC CAC GTA CCT CAG GCT CAT GTA	3271
Ala Tyr Thr Thr Pro Pro His Met Ala His Val Pro Gln Ala His Val	
1060 1065 1070	
CAG TCA GGA ATG GTT CCT TCT CAT CCA ACT GCC CAT GCG CCA ATG ATG	3319
Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro Met Met	
1075 1080 1085 1090	
CTA ATG ACG ACA CAG CCA CCC GGT CCC AAG GCC GCC CTC GCT CAA AGT	3367
Leu Met Thr Thr Gln Pro Pro Gly Pro Lys Ala Ala Leu Ala Gln Ser	
1095 1100 1105	
GCA CTA CAG CCC ATT CCA GTT TCG ACA ACA GCG CAT TTC CCT TAT ATG	3415
Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro Tyr Met	
1110 1115 1120	

ACG CAC CCT TCA GTA CAA GCC CAC CAC CAA CAG CAG TTG TAA 3457
 Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu
 1125 1130 1135
 GGCTGCCTTG GAGGAACCGA AAGGCCAAAT CCCTTCTTCC CTTCTCTGCT TCTGCCAACC 3517
 GGAAGCACAG AAAACTAGAA CTTCAATTGAT TTTGTTTTTTT AAAAGATACA CTGATTTAAC 3577
 ATCTGATAGG AATGCTAACA GCTCACTTGC AGTGGAGGAT GTTTTGGACC GAGTAGAGGC 3637
 ATGTAGGGAC TTGTGGCTGT TCCATAATTC CATGTGCTGT TGCAGGGTCC TGCAAGTACC 3697
 CAGCTCTGCT TGCTGAAACT GGAAGTTATT TATTTTTTTAA TGGCCCTTGA GAGTCATGAA 3757
 CACATCAGCT AGCAACAGAA GTAACAAGAG TGATTCTTGC T 3798

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ser Leu Lys Pro Gln Pro Gln Pro Pro Ala Pro Ala Thr Gly Arg
 1 5 10 15
 Lys Pro Gly Gly Gly Leu Leu Ser Ser Pro Gly Ala Ala Pro Ala Ser
 20 25 30
 Ala Ala Val Thr Ser Ala Ser Val Val Pro Ala Pro Ala Ala Pro Val
 35 40 45
 Ala Ser Ser Ser Ala Ala Ala Gly Gly Gly Arg Pro Gly Leu Gly Arg
 50 55 60
 Gly Arg Asn Ser Ser Lys Gly Leu Pro Gln Pro Thr Ile Ser Phe Asp
 65 70 75 80
 Gly Ile Tyr Ala Asn Val Arg Met Val His Ile Leu Thr Ser Val Val
 85 90 95
 Gly Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly
 100 105 110
 Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala
 115 120 125
 His Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg Glu Glu Ile
 130 135 140
 Met Glu Ser Val Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe
 145 150 155 160

Lys Asp Thr Asp Ser Ser Tyr Ala Arg Arg Asp Ala Phe Thr Asp Ser
 165 170 175
 Ala Leu Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu
 180 185 190
 Pro Trp Asp Ala Gly Glu Leu Thr Ala Ser Glu Glu Leu Glu Leu Glu
 195 200 205
 Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn
 210 215 220
 Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser
 225 230 235 240
 Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg
 245 250 255
 Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln
 260 265 270
 Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu
 275 280 285
 Lys Tyr Thr Ala Val Gln Arg Asn Cys Ser Asp Arg Glu Gly His Gly
 290 295 300
 Pro Asn Thr Arg Asp Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg
 305 310 315 320
 Glu Val Leu Ser Trp Gly Ser Gly Arg Gln Ser Ser Pro Arg Met Gly
 325 330 335
 Gln Pro Gly Pro Gly Ser Met Pro Ser Arg Ala Ala Ser His Thr Ser
 340 345 350
 Asp Phe Asn Pro Asn Ala Gly Ser Asp Gln Arg Val Val Asn Gly Gly
 355 360 365
 Val Pro Trp Pro Ser Pro Cys Pro Ser His Ser Ser Arg Pro Pro Ser
 370 375 380
 Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr His
 385 390 395 400
 Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser
 405 410 415
 His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys
 420 425 430
 Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg
 435 440 445
 His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Met Ser Ser
 450 455 460

Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala Ala Pro
 465 470 475 480
 Pro Val Ala Arg Thr Ser Pro Ala Gly Gly Thr Trp Ser Ser Val Val
 485 490 495
 Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro
 500 505 510
 Arg Gln Ser Ser Ile Gly Asn Ser Pro Ser Gly Pro Val Leu Ala Ser
 515 520 525
 Pro Gln Ala Gly Ile Ile Pro Ala Glu Ala Val Ser Met Pro Val Pro
 530 535 540
 Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala Leu Thr
 545 550 555 560
 Pro Ser Ile Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg Gln Asn
 565 570 575
 Ser Pro Ala Gly Ser Lys Glu Asn Val Lys Ala Ser Glu Thr Ser Pro
 580 585 590
 Ser Phe Ser Lys Ala Asp Asn Lys Gly Met Ser Pro Val Val Ser Glu
 595 600 605
 His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp Phe Arg
 610 615 620
 Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu Ser Lys
 625 630 635 640
 Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys Thr Glu
 645 650 655
 Ala Ser Ala Lys Asp Ser Phe Ile Asp Ser Ser Ser Ser Ser Asn
 660 665 670
 Cys Thr Ser Gly Ser Ser Lys Thr Asn Ser Pro Ser Ile Ser Pro Ser
 675 680 685
 Met Leu Ser Asn Ala Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln
 690 695 700
 Gly Val Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Arg
 705 710 715 720
 Glu Glu Lys Lys Asp Thr Thr Glu Gln Val Arg Lys Ser Thr Leu Asn
 725 730 735
 Pro Asn Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro
 740 745 750
 Ser Thr Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser
 755 760 765

Met Val Gly His Gln Gln Pro Ala Pro Val Tyr Thr Gln Pro Val Cys
770 775 780

Phe Ala Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln
785 790 795 800

Pro Leu Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys
805 810 815

Thr Tyr Arg Ala Gly Lys Val Pro Asn Met Pro Gln Gln Arg Gln Asp
820 825 830

Gln His His Gln Ser Thr Met Met His Pro Ala Ser Ala Ala Gly Pro
835 840 845

Pro Ile Val Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr
850 855 860

Ser Pro Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His
865 870 875 880

Tyr Gln Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn
885 890 895

Ala Arg Met Met Ala Pro Pro Ala His Ala Gln Pro Gly Leu Val Ser
900 905 910

Ser Ser Ala Ala Gln Phe Gly Ala His Glu Gln Thr His Ala Met Tyr
915 920 925

Ala Cys Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr
930 935 940

Phe Ala Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn
945 950 955 960

Ala Ala Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro
965 970 975

Thr Gly Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser
980 985 990

Pro Val Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala
995 1000 1005

Ser Pro Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr
1010 1015 1020

Pro Pro Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Ser Ser
1025 1030 1035 1040

Phe Pro Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val
1045 1050 1055

Gln Pro Ala Tyr Thr Thr Pro Pro His Met Ala His Val Pro Gln Ala
1060 1065 1070

His Val Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro
1075 1080 1085

Met Met Leu Met Thr Thr Gln Pro Pro Gly Pro Lys Ala Ala Leu Ala
1090 1095 1100

Gln Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro
1105 1110 1115 1120

Tyr Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu
1125 1130 1135

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGCCCCTCA CCATGTCG

18

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGGCTTGCG GACATTGG

18

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGCGGCTGC CAATGTCC

18

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTAACCGTTC GGCGCCCG

18

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGCTCCCGGC GGCTCCTT

18

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCTGCTGCT GCTGGGGCTT CAG

23

(2) INFORMATION FOR SEQ ID NO:12:

- A1*
Cont.
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
CCGCCCCTC CTCACGTGT

19

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
ACCCCCGAGA AAGCAACC

18

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
CCGTTGCCGT TGCTACCA

18

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTCTCATGTG CGGCATCAAG

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val	Tyr	Gly	Pro	Leu	Thr	Met	Ser	Leu	Lys	Pro	Gln	Gln	Gln	Gln	Gln	
1				5					10						15	
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	
				20				25						30		
Gln	Pro	Pro	Pro	Ala	Ala	Ala	Asn	Val	Arg	Lys	Pro	Gly	Gly	Ser	Gly	
				35			40					45				
Leu	Leu	Ala	Ser	Pro	Ala	Ala	Ala	Pro	Ser	Pro	Ser	Ser	Ser	Ser	Val	
				50			55				60					
Ser	Ser	Ser	Ser	Ala	Thr	Ala	Pro	Ser	Ser	Val	Val	Ala	Ala	Thr	Ser	
65					70					75				80		
Gly	Gly	Gly	Arg	Pro	Gly	Leu	Gly	Arg	Gly	Arg	Asn	Ser	Asn	Lys	Gly	
				85				90						95		
Leu	Pro	Gln	Ser	Thr	Ile	Ser	Phe	Asp	Gly	Ile	Tyr	Ala	Asn	Met	Arg	
				100				105					110			
Met	Val	His	Ile	Leu	Thr	Ser	Val	Val	Gly	Ser	Lys	Cys	Glu	Val	Gln	
				115			120					125				
Val	Lys	Asn	Gly	Gly	Ile	Tyr	Glu	Gly	Val	Phe	Lys	Thr	Tyr	Ser	Pro	
				130			135				140					
Lys	Cys	Asp	Leu	Val	Leu	Asp	Ala	Ala	His	Glu	Lys	Ser	Thr	Glu	Ser	
145					150					155				160		
Ser	Ser	Gly	Pro	Lys	Arg	Glu	Glu	Ile	Met	Glu	Ser	Ile	Leu	Phe	Lys	
				165					170					175		
Cys	Ser	Asp	Phe	Val	Val	Val	Gln	Phe	Lys	Asp	Met	Asp	Ser	Ser	Tyr	
				180				185					190			

Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala Ile Ser Ala Lys Val Asn
 195 200 205
 Gly Glu His Lys Glu Lys Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu
 210 215 220
 Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu Asn Asp Val Ser Asn Gly
 225 230 235 240
 Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val
 245 250 255
 Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu
 260 265 270
 Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln
 275 280 285
 Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala
 290 295 300
 Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln
 305 310 315 320
 Arg Asn Ser Ser Glu Arg Glu Gly His Ser Ile Asn Thr Arg Glu Asn
 325 330 335
 Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg
 340 345

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 326 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

His Glu Gly Pro Leu Thr Met Ser Leu Lys Pro Gln Pro Gln Pro Pro
 1 5 10 15
 Ala Pro Ala Thr Gly Arg Lys Pro Gly Gly Gly Leu Leu Ser Ser Pro
 20 25 30
 Gly Ala Ala Pro Ala Ser Ala Ala Val Thr Ser Ala Ser Val Val Pro
 35 40 45
 Ala Pro Ala Ala Pro Val Ala Ser Ser Ser Ala Ala Ala Gly Gly Gly
 50 55 60

Q1
Cont.

Arg	Pro	Gly	Leu	Gly	Arg	Gly	Arg	Asn	Ser	Ser	Lys	Gly	Leu	Pro	Gln	65	70	75	80
Pro	Thr	Ile	Ser	Phe	Asp	Gly	Ile	Tyr	Ala	Asn	Val	Arg	Met	Val	His	85	90	95	
Ile	Leu	Thr	Ser	Val	Val	Gly	Ser	Lys	Cys	Glu	Val	Gln	Val	Lys	Asn	100	105	110	
Gly	Gly	Ile	Tyr	Glu	Gly	Val	Phe	Lys	Thr	Tyr	Ser	Pro	Lys	Cys	Asp	115	120	125	
Leu	Val	Leu	Asp	Ala	Ala	His	Glu	Lys	Ser	Thr	Glu	Ser	Ser	Ser	Gly	130	135	140	
Pro	Lys	Arg	Glu	Glu	Ile	Met	Glu	Ser	Val	Leu	Phe	Lys	Cys	Ser	Asp	145	150	155	160
Phe	Val	Val	Val	Gln	Phe	Lys	Asp	Thr	Asp	Ser	Ser	Tyr	Ala	Arg	Arg	165	170	175	
Asp	Ala	Phe	Thr	Asp	Ser	Ala	Leu	Ser	Ala	Lys	Val	Asn	Gly	Glu	His	180	185	190	
Lys	Glu	Lys	Asp	Leu	Glu	Pro	Trp	Asp	Ala	Gly	Glu	Leu	Thr	Ala	Ser	195	200	205	
Glu	Glu	Leu	Glu	Leu	Glu	Asn	Asp	Val	Ser	Asn	Gly	Trp	Asp	Pro	Asn	210	215	220	
Asp	Met	Phe	Arg	Tyr	Asn	Glu	Glu	Asn	Tyr	Gly	Val	Val	Ser	Thr	Tyr	225	230	235	240
Asp	Ser	Ser	Leu	Ser	Ser	Tyr	Thr	Val	Pro	Leu	Glu	Arg	Asp	Asn	Ser	245	250	255	
Glu	Glu	Phe	Leu	Lys	Arg	Glu	Ala	Arg	Ala	Asn	Gln	Leu	Ala	Glu	Glu	260	265	270	
Ile	Glu	Ser	Ser	Ala	Gln	Tyr	Lys	Ala	Arg	Val	Ala	Leu	Glu	Asn	Asp	275	280	285	
Asp	Arg	Ser	Glu	Glu	Glu	Lys	Tyr	Thr	Ala	Val	Gln	Arg	Asn	Cys	Ser	290	295	300	
Asp	Arg	Glu	Gly	His	Gly	Pro	Asn	Thr	Arg	Asp	Asn	Lys	Tyr	Ile	Pro	305	310	315	320
Pro	Gly	Gln	Arg	Asn	Arg											325			

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

ai
cont
(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Ala Pro Gln Pro Pro Pro Pro Gln Gln His Gln Glu Arg Pro Gly
1 5 10 15
Ala Ala Ala Ile Gly Ser Ala Arg Gly Gln Ser Thr Gly Lys Gly Pro
20 25 30
Pro Gln Ser Pro Val Phe Glu Gly Val Tyr Asn Asn Ser Arg Met Leu
35 40 45
His Phe Leu Thr Ala Val Val Gly Ser Thr Cys Asp Val Lys Val Lys
50 55 60
Asn Gly Thr Thr Tyr Glu Gly Ile Phe Lys Thr Leu Ser Ser Lys Phe
65 70 75 80
Glu Leu Ala Val Asp Ala Val His Arg Lys Ala Ser Glu Pro Ala Gly
85 90 95
Gly Pro Arg Arg Glu Asp Ile Val Asp Thr Met Val Phe Lys Pro Ser
100 105 110
Asp Val Met Leu Val His Phe Arg Asn Val Asp Phe Asn Tyr Ala Thr
115 120 125
Lys Asp Lys Phe Thr Asp Ser Ala Ile Ala Met Asn Ser Lys Val Asn
130 135 140
Gly Glu His Lys Glu Lys Val Leu Gln Arg Trp Glu Gly Gly Asp Ser
145 150 155 160
Asn Ser Asp Asp Tyr Asp Leu Glu Ser Asp Met Ser Asn Gly Trp Asp
165 170 175
Pro Asn Glu Met Phe Lys Phe Asn Glu Glu Asn Tyr Gly Val Lys Thr
180 185 190
Thr Tyr Asp Ser Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Lys Asp
195 200 205
Asn Ser Glu Glu Phe Arg Gln Arg Glu Leu Arg Ala Ala Gln Leu Ala
210 215 220
Arg Glu Ile Glu Ser Ser Pro Gln Tyr Arg Leu Arg Ile Ala Met Glu
225 230 235 240
Asn Asp Asp Gly Arg Thr Glu Glu Glu Lys His Ser Ala Val Gln Arg
245 250 255
Gln Gly Ser Gly Arg Glu Ser Pro Ser Leu Ala Ser Arg Glu Gly Lys
260 265 270

Al
Conclude

Tyr Ile Pro
275